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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification <sup>6</sup> : <b>C12N 15/12, C07K 14/72, 16/28, C12P 19/34, G01N 33/58</b>		A1	(11) International Publication Number: <b>WO 00/00606</b> (43) International Publication Date: <b>6 January 2000 (06.01.00)</b>
(21) International Application Number: <b>PCT/AU99/00523</b>		(81) Designated States: AU, CA, JP, US, European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
(22) International Filing Date: <b>29 June 1999 (29.06.99)</b>		Published <i>With international search report.</i>	
(30) Priority Data: <b>PP 4385 29 June 1998 (29.06.98) AU</b>			
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(54) Title: NPY-Y7 RECEPTOR GENE

(57) Abstract

The invention provides isolated polynucleotide molecules encoding a novel neuropeptide Y (NPY) receptor (designated NPY-Y7). These isolated polynucleotide molecules can be used to express the receptor in cells which can then be used to screen compounds for agonist and antagonist activity.

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## NPY-Y7 RECEPTOR GENE

### Field of Invention:

5 The present invention relates to isolated polynucleotide molecules which encode a novel neuropeptide Y (NPY) receptor designated NPY-Y7. In addition, the present invention relates to the use of these molecules in the production of NPY-Y7 receptors using recombinant DNA technology and to methods of screening and testing compounds for agonist or antagonist activity.

10

### Background of the Invention:

15 Neuropeptide Y (NPY) forms a family (called the pancreatic polypeptide family) together with pancreatic polypeptide (PP) and peptide YY (PYY), which all consist of 36 amino acids and possess a common tertiary structure. NPY receptors, members of the G protein-coupled receptor superfamily, when activated influence a diverse range of important physiological parameters, including effects on psychomotor activity, central endocrine secretion, anxiety, reproduction, vasoactive effects on the cardiovascular system and strongly stimulates food consumption. Specific 20 agonists and antagonists of NPY are therefore likely to be of substantial benefit for therapy of a wide range of clinical disorders. As NPY possess a compact tertiary structure and different parts of the molecule are required for interaction with different subtypes of the receptor, the logical developments of both agonists and antagonists is critically dependent upon the availability 25 and knowledge of specific receptor structure.

30 It is presently known that NPY binds specifically to at least six receptors; Y1, Y2, Y3, Y4, Y5 (or "atypical Y1") and Y6. While it has been demonstrated that NPY receptors couple to the adenylate cyclase second messenger system, it remains probable that additional NPY receptor subtypes exist since there is evidence that phosphatidylinositol turnover, cations, and arachidonic acid may also function as second messengers for NPY.

35 Since NPY agonists and antagonists may have commercial value as, for example, potential anti-hypertensive agents, cardiovascular drugs, neuronal growth factors, anti-psychotics, anti-obesity and anti-diabetic agents, the ability to produce NPY receptors by recombinant DNA technology would be

advantageous. To this end, DNA molecules encoding Y1, Y2, Y4, Y5 and Y6 have previously been isolated.

The present inventors have now isolated novel DNA molecules encoding the human and murine NPY-Y7 receptors.

5

#### Summary of the Invention:

Thus, in a first aspect, the present invention provides an isolated polynucleotide molecule encoding an NPY-Y7 receptor or a functionally equivalent fragment thereof.

10 The encoded NPY-Y7 receptor is characterised by the N-terminal amino acid sequence:

$MX_1X_2MX_3EKWDX_4NSSE$  (SEQ ID NO: 1),

wherein  $X_1$ ,  $X_2$ ,  $X_3$  and  $X_4$  are selected from codable amino acids but, preferably,  $X_1$  is selected from Phe and Ser,  $X_2$  is selected from Ile and Thr,  $X_3$  is selected from Asn and Ser, and  $X_4$  is selected from Thr and Ser.

15 More preferably, the polynucleotide molecule encodes a human NPY-Y7 receptor of about 408 amino acids or a murine NPY-Y7 receptor of about 405 amino acids.

20 Most preferably, the polynucleotide molecule encodes a human NPY-Y7 receptor having an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 2 or a murine NPY-Y7 receptor having an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 3.

25 The polynucleotide molecule may comprise a nucleotide sequence substantially corresponding or, at least, showing at least 90% (more preferably, at least 95%) homology to that shown at nucleotides 1 to 1903 or nucleotides 369 to 1592 of SEQ ID NO: 4 or any portion thereof encoding a functionally equivalent NPY-Y7 receptor fragment.

30 The polynucleotide molecule may be incorporated into plasmids or expression vectors (including viral vectors), which may then be introduced into suitable bacterial, yeast, insect and mammalian host cells. Such host cells may be used to express the NPY-Y7 receptor.

Accordingly, in a second aspect, the present invention provides a mammalian, insect, yeast or bacterial host cell transformed with the polynucleotide molecule of the first aspect.

35 In a third aspect, the present invention provides a method of producing NPY-Y7 receptors or functionally equivalent fragments thereof, comprising

culturing the host cell of the second aspect under conditions enabling the expression of NPY-Y7 receptors or functionally equivalent fragments thereof.

5 Preferably, the host cell is mammalian or of insect origin. Where the cell is mammalian, it is presently preferred that it be a Chinese hamster ovary (CHO) cell, monkey kidney (COS) cell or human embryonic kidney 293 cell. Where the cell is of insect origin, it is presently preferred that it be an insect Sf9 cell.

10 In a preferred embodiment, the NPY-Y7 receptors or functionally equivalent fragments thereof are expressed onto the surface of the host cell.

15 The polynucleotide molecule of the present invention encodes an NPY receptor which may be of interest both clinically and commercially as it is expressed in many regions of the body and neuropeptides of the NPY family affect a wide number of systems.

20 By using the polynucleotide molecule of the present invention it is possible to obtain NPY-Y7 receptor protein or fragments thereof in a substantially pure form.

25 Accordingly, in a fourth aspect, the present invention provides a NPY-Y7 receptor or a functionally equivalent fragment of said receptor, in a substantially pure form.

30 In a fifth aspect, the present invention provides an antibody or fragment thereof capable of specifically binding to the NPY-Y7 receptor or functionally equivalent fragment of the fourth aspect.

35 In a sixth aspect, the present invention provides a non-human animal transformed with the polynucleotide molecule of the first aspect of the present invention.

40 In a seventh aspect, the present invention provides a method for detecting agonist or antagonist agents of an NPY-Y7 receptor, comprising contacting an NPY-Y7 receptor, functionally equivalent fragment thereof or a cell transfected with and expressing the polynucleotide molecule of the first aspect, with a test agent under conditions enabling the activation of an NPY-Y7 receptor, and detecting an increase or decrease in activity of the NPY-Y7 receptor or functionally equivalent fragment thereof.

45 An increase or decrease in activity of the receptor or functionally equivalent fragment thereof may be detected by measuring changes in cAMP production,  $Ca^{2+}$  levels or IP3 turnover after activating the receptor or fragment with specific agonist or antagonist agents.

In a further aspect, the present invention provides an oligonucleotide or polynucleotide probe comprising a nucleotide sequence of 10 or more nucleotides, the probe comprising a nucleotide sequence such that the probe specifically hybridises to the polynucleotide molecule of the first aspect under high stringency conditions (Sambrook et al., *Molecular Cloning: a laboratory manual*, Second Edition, Cold Spring Harbor Laboratory Press).

In a still further aspect, the present invention provides an antisense oligonucleotide or polynucleotide molecule comprising a nucleotide sequence capable of specifically hybridising to an mRNA molecule which encodes an NPY-Y7 receptor so as to prevent translation of the mRNA molecule.

Such antisense oligonucleotide or polynucleotide molecules may include a ribozyme region to catalytically inactivate mRNA to which it is hybridised.

The polynucleotide molecule of the first aspect of the invention may be a dominant negative mutant which encodes a gene product causing an altered phenotype by, for example, reducing or eliminating the activity of endogenous NPY-Y7 receptors.

The term "substantially corresponding" as used herein in relation to amino acid sequences is intended to encompass minor variations in the amino acid sequences which do not result in a decrease in biological activity of the NPY-Y7 receptor. These variations may include conservative amino acid substitutions. The substitutions envisaged are:-

G, A, V, I, L, M; D, E; N, Q; S, T; K, R, H; F, Y, W, H; and P,  $\text{N}\alpha$ -alkalamino acids.

The term "substantially corresponding" as used herein in relation to nucleotide sequences is intended to encompass minor variations in the nucleotide sequences which due to degeneracy in the DNA code do not result in a change in the encoded protein. Further, this term is intended to encompass other minor variations in the sequence which may be required to enhance expression in a particular system but in which the variations do not result in a decrease in biological activity of the encoded protein.

The term "functionally equivalent fragment/s" as used herein is intended to refer to fragments of the NPY-Y7 receptor that exhibit binding specificity and activity that is substantially equivalent to the NPY-Y7 receptor from which it/they is/are derived.

5        The terms "comprise", "comprises" and "comprising" as used throughout the specification are intended to refer to the inclusion of a stated step, component or feature or group of steps, components or features with or without the inclusion of a further step, component or feature or group of steps, components or features.

10       Reference to percent homology made in this specification have been calculated using the BLAST program blastn as described by Altschul, S.F. et al., "Capped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Research*, Vol. 25, No. 17, pp. 3389-3402 (1997).

**Brief description of the accompanying Figures:**

15       Figure 1 shows the degree of identity between the predicted amino acid sequence of the human NPY-Y1, NPY-Y2 and NPY-Y7 receptors.

20       Figure 2 provides a graph showing the inhibition of human [<sup>125</sup>I]PYY binding with various NPY-related peptides on human NPY-Y7 membranes. The results were obtained through competitive displacement of [<sup>125</sup>I]PYY on membranes of COSm6 cells transiently expressing human NPY-Y7 receptors. Membranes were incubated with [<sup>125</sup>I]PYY (50pM) and increasing concentrations of peptide competitors. Data are representative of a single experiment with each point measured in triplicate.

25       Figure 3 provides a schematic diagram of the murine NPY-Y7 receptor gene. The gene covers approximately 12 kb and consists of three exons.

30       Figure 4 shows the degree of identity between the predicted amino acid sequence of the human and murine NPY-Y7 receptors.

**Detailed Disclosure of the Invention:**

**Human NPY-Y7 cDNA**

35       Human amygdala and testis cDNA libraries (Stratagene) were screened under low stringency conditions with a 401 bp <sup>32</sup>P-labelled fragment (corresponding to nucleotides 507 to 908 of SEQ ID NO: 4) originated from a human fetal brain EST clone (GenBank AA449919). Two overlapping cDNA clones were obtained from the screen. The combined nucleotide sequence (hy7) of the clones is shown as SEQ ID NO: 4 and encodes a protein of 408 amino acids (SEQ ID NO: 2).

Sequence comparison with other G protein coupled receptors identified neuropeptide Y receptors as the most closely related group with approximately 32% amino acid sequence identity to the Y1 receptor subtype (Figure 1). Further, *in situ* hybridisation studies of rat brain sections has identified a NPY-Y7 mRNA distribution (expression was found to occur in the amygdala, the CA3 region of the hippocampus and the piriform cortex) which is consistent with the expression of other NPY-receptor subtypes (Blomquist, A.G., and Herzog, H., TINS 20(7), 1997) and is in agreement with the suggestions of the existence of further Y-receptor family members. This mRNA distribution suggests important functions for the NPY-Y7 receptor in the regulation of the circadian rhythm, anxiety and metabolic status.

Radio-ligand binding experiments has shown that the protein encoded by the hy7 cDNA shows highest affinity for human PYY (Figure 2). These experiments were conducted using COS-6 or HEK (293) cells transiently expressing recombinant Y7 receptor protein. The radio-ligand binding (Herzog, H. et al., Proc. Natl. Acad. Sci. USA 89:5794-5798, 1992) suggests that the NPY-Y7 receptor has a pharmacology similar to the Y2 receptor (Rose, P., J. Biol. Chem. 270:22661-22664, 1995). The rank of potency for the Y7 receptor is:

20 PYY>NPY>[2-36]PYY>[3-36]NPY>[13-36]NPY>>(Leu31, Pro34)NPY>PP.

#### Chromosomal Localisation of the Human Y7 gene

Screening of a medium resolution Stanford G3 panel of 83 clones was performed to further refine the map position of the hy7 gene. PCR amplification was carried out on this panel using primers hy7-A (5'GGATGGCCATTGGAAAC3') and hy7-B (5'CCAATCCTTCCATACATG3'), corresponding to nucleotides 507-524 and 890-907 of the hy7 cDNA (SEQ ID NO: 4), respectively. The analysis indicated that the hy7 gene is most closely associated with the marker SHGC-418 on the long arm of chromosome 4. This map location is defined by markers AFM191xh2 and AFM347ZH1. Assessment of the flanking markers using the Whitehead/MIT STS-Based Map of the Human Genome ([http://www-genome.wi.mit.edu/cgi-bin/contig/phys\\_map](http://www-genome.wi.mit.edu/cgi-bin/contig/phys_map)) in conjunction with The Genome Directory (Adams, M.D., et al. Nature 377 Suppl. (1995)) identifies 4q21.3 as the most likely position of the hy7 gene.

Mouse Y7 genomic DNA

Using a  $^{32}\text{P}$ -labelled fragment of the hy7 cDNA a mouse genomic BAC library (Genome Systems) was screened. A clone encoding the entire gene of the mouse equivalent to hy7 was isolated (SEQ ID NO: 5). The gene covers approximately 12 kb and is divided by two introns into three exons (Figure 5). Figure 4 shows the degree of identity between the predicted amino acid sequence of the human and murine NPY-Y7 receptors.

Pharmacological characterisation

pcDNA3.1-hy7 cDNA was transiently transfected into the COSm6 cell line using FUGENE and 5mg of DNA/106 cells. The COSm6 cells were grown in Dulbecco's modified Eagles medium supplemented with 2mM glutamine and 10% fetal calf serum, in 5%  $\text{CO}_2$  at 37°C. Membranes were harvested with COSm6 cells 72hr post-transfection. Adherent cells were washed twice in ice-cold phosphate buffered saline and lysed using a glass homogeniser in ice-cold hypotonic buffer (50mM Tris-HCl, pH 7.4, 0.1% bacitracin). Membranes were pelleted by high speed centrifugation (30,000 x g, 15 min, 4°C), homogenised again in ice-cold hypotonic buffer and collected again by high speed centrifugation (30,000 x g, 15 min, 4°C). The final membrane pellet was resuspended into 1ml of ice-cold binding buffer (50mM Tris-HCl, pH 7.4, 10mM NaCl, 5mM  $\text{MgCl}_2$ , 2.5mM  $\text{CaCl}_2$ , 0.1% bacitracin, 0.1% bovine serum albumin. Membrane suspensions were diluted in binding buffer to yield membrane protein concentrations of 0.05mg/ml. Under these conditions non-specific binding of [ $^{125}\text{I}$ ]PYY to membranes was less than 10%. [ $^{125}\text{I}$ ]PYY and unlabelled peptide competitors were also diluted to the required concentrations in binding buffer. Samples were prepared by mixing 50ml binding buffer, unlabelled peptide or binding buffer (50ml), [ $^{125}\text{I}$ ]PYY (50mM, 50ml) and membrane suspension (100ml). Samples were incubated at room temperature for 2hr. Incubations were terminated by centrifugation (4min) and pellets collected. Radioactivity was measured for 1min in a g counter.

It will be appreciated by persons skilled in the art that numerous variations and/or modifications may be made to the invention as shown in the specific embodiments without departing from the spirit or scope of the invention as broadly described. The present embodiments are, therefore, to be considered in all respects as illustrative and not restrictive.

Claims:

1. An isolated polynucleotide molecule encoding an NPY-Y7 receptor or a functionally equivalent fragment thereof, wherein the encoded NPY-Y7 receptor is characterised by the N-terminal amino acid sequence:  
5  $MX_1X_2MX_3EKWDX_4NSSE$  (SEQ ID NO: 1),  
wherein  $X_1$ ,  $X_2$ ,  $X_3$  and  $X_4$  are selected from codable amino acids.
2. A polynucleotide molecule according to claim 1, wherein  $X_1$  is selected from Phe and Ser,  $X_2$  is selected from Ile and Thr,  $X_3$  is selected from Asn and Ser and  $X_4$  is selected from Thr and Ser.  
10
3. A polynucleotide molecule according to claim 1 or 2, wherein the polynucleotide molecule encodes an NPY-Y7 receptor of human origin of about 408 amino acids in length.  
15
4. A polynucleotide molecule according to claim 3, wherein the polynucleotide molecule encodes a human NPY-Y7 receptor having an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 2.  
20
5. A polynucleotide molecule according to claim 1 or 2, wherein the polynucleotide molecule encodes an NPY-Y7 receptor of murine origin of about 405 amino acids in length.  
25
6. A polynucleotide molecule according to claim 5, wherein the polynucleotide molecule encodes a murine NPY-Y7 receptor having an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 3.  
30
7. A polynucleotide molecule encoding an NPY-Y7 receptor, wherein the polynucleotide molecule comprises a nucleotide sequence showing at least 90% homology to that shown at nucleotides 1 to 1903 or nucleotides 369 to 1592 of SEQ ID NO: 4 or any portion thereof encoding a functionally equivalent NPY-Y7 receptor fragment.

8. A polynucleotide molecule according to claim 7, wherein the polynucleotide molecule comprises a nucleotide sequence showing at least 95% homology to that shown at nucleotides 1 to 1903 or nucleotides 369 to 1592 of SEQ ID NO: 4 or any portion thereof encoding a functionally equivalent NPY-Y7 receptor fragment.

9. A polynucleotide molecule according to claim 7 or 8, wherein the polynucleotide molecule comprises a nucleotide sequence substantially corresponding to that shown at nucleotides 1 to 1903 or nucleotides 369 to 1592 of SEQ ID NO: 4 or any portion thereof encoding a functionally equivalent NPY-Y7 receptor fragment.

10. A plasmid or expression vector including a polynucleotide molecule according to any one of claims 1 to 9.

11. A host cell transformed with a polynucleotide molecule according to any one of claims 1 to 9 or a plasmid or expression vector according to claim 10.

12. A host cell according to claim 11, wherein the cell is a mammalian or insect cell.

13. A host cell according to claim 12, wherein the cell is a Chinese hamster ovary (CHO) cell, human embryonic kidney (HEK) 293 cell or an insect Sf9 cell.

14. A host cell according to any one of claims 11 to 13, wherein the cell expresses the NPY-Y7 receptor or functionally equivalent fragment thereof onto the cell's surface.

15. An NPY-Y7 receptor which is characterised by the N-terminal amino acid sequence:

MX<sub>1</sub>X<sub>2</sub>MX<sub>3</sub>EKWDX<sub>4</sub>NSSE (SEQ ID NO:1),

wherein X<sub>1</sub>, X<sub>2</sub>, X<sub>3</sub> and X<sub>4</sub> are selected from codable amino acids, or a functionally equivalent fragment of said receptor, in a substantially pure form.

- 5 16. A receptor according to claim 15, wherein said receptor is a human receptor of about 408 amino acids.
17. A receptor according to claim 16, wherein said receptor has an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 2.
- 10 18. A receptor according to claim 15, wherein said receptor is a murine receptor of about 405 amino acids.
- 15 19. A receptor according to claim 18, wherein the receptor has an amino acid sequence substantially corresponding to that shown as SEQ ID NO: 3.
- 20 20. An antibody or fragment thereof which specifically binds to an NPY-Y7 receptor according to any one of claims 15 to 19.
- 25 21. A non-human animal transformed with a polynucleotide molecule according to any one of claims 1 to 9 or a plasmid or expression vector according to claim 10.
22. A method for detecting agonist or antagonist agents of an NPY-Y7 receptor, comprising contacting an NPY-Y7 receptor according to any one of claims 15 to 19 or a host cell transformed according to any one of claims 11 to 14, with a test agent under conditions enabling the activation of said receptor, and detecting an increase or decrease in the receptor activity.
- 30 23. An oligonucleotide or polynucleotide probe comprising a nucleotide sequence of 10 or more nucleotides, the probe comprising a nucleotide sequence such that the probe specifically hybridises to the polynucleotide molecule according to any one of claims 1 to 9 under high stringency conditions.

24. An antisense oligonucleotide or polynucleotide molecule comprising a nucleotide sequence capable of specifically hybridising to an mRNA molecule which encodes an NPY-Y7 receptor encoded by the polynucleotide molecule according to any one of claims 1 to 9, so as to prevent translation of the mRNA molecule.

5

25. A method of producing NPY-Y7 receptors or functionally equivalent fragments thereof according to any one of claims 15 to 19, comprising culturing a host cell according to any one of claims 11 to 14 under conditions enabling the expression of NPY-Y7 receptors or functionally equivalent fragments thereof, and optionally recovering the receptors or functionally equivalent fragments thereof.

10

Sequence Listings:

Applicant: Garvan Institute of Medical Research  
Title of Invention: NPY-Y7 Receptor Gene

Prior Application Number: PP 4385  
Prior Application Filing Date: 1998-06-29

Number of SEQ ID NOS: 5

Software: PatentIn Ver. 2.1

SEQ ID NO: 1  
Length: 14  
Type: PRT  
Organism: Artificial Sequence

Feature:

Other Information: Description of Artificial Sequence: N-terminal  
consensus sequence

Sequence: 1  
Met Xaa Xaa Met Xaa Glu Lys Trp Asp Xaa Asn Ser Ser Glu  
1 5 10

SEQ ID NO: 2  
Length: 408  
Type: PRT  
Organism: Homo sapiens

Sequence: 2  
Met Phe Ile Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp  
1 5 10 15  
His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp  
20 25 30  
Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala  
35 40 45  
Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met

50	55	60
Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His		
65	70	75
Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu		
85	90	95
Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala		
100	105	110
Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln		
115	120	125
Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val		
130	135	140
Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile		
145	150	155
Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr		
165	170	175
Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr		
180	185	190
Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp		
195	200	205
Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr		
210	215	220
Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile		
225	230	235
Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His		
245	250	255
Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys		
260	265	270
Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu		
275	280	285
Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp		
290	295	300
Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe		
305	310	315
Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr		
325	330	335
Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln		
340	345	350
Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu		
355	360	365

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Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln  
           370                  375                  380  
 Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys  
           385                  390                  395                  400  
 Ser Ala Glu Asn Pro Asn Arg Asn  
                           405

SEQ ID NO: 3

Length: 405

Type: PRT

Organism: Mus musculus

Sequence: 3

Met Ser Thr Met Ser Glu Lys Trp Asp Ser Asn Ser Ser Glu Ser Trp  
   1                  5                  10                  15  
 Asn His Ile Trp Ser Gly Asn Asp Thr Gln His His Trp Tyr Ser Asp  
   20                  25                  30  
 Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala  
   35                  40                  45  
 Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val  
   50                  55                  60  
 Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His  
   65                  70                  75                  80  
 Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu  
   85                  90                  95  
 Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala  
   100                 105                 110  
 Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln  
   115                 120                 125  
 Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val  
   130                 135                 140  
 Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val  
   145                 150                 155                 160  
 Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala  
   165                 170                 175  
 Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr  
   180                 185                 190  
 Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp

195	200	205
Cys Arg Glu Asp Trp Pro Arg His Glu Met Arg Arg Ile Tyr Thr Thr		
210	215	220
Val Leu Phe Ala Ile Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile		
225	230	235
Met Tyr Ala Arg Ile Gly Ala Ser Leu Phe Lys Thr Ala Ala His Cys		
245	250	255
Thr Gly Lys Gln Arg Pro Val Gln Cys Met Tyr Gln Glu Lys Gln Lys		
260	265	270
Val Ile Lys Met Leu Leu Thr Val Ala Leu Leu Phe Ile Leu Ser Trp		
275	280	285
Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Thr Asp Leu Ser		
290	295	300
Pro Asn Lys Leu Arg Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His		
305	310	315
Trp Leu Ala Phe Cys Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe		
325	330	335
Phe Asn Glu Asn Phe Arg Asn Gly Phe Gln Asp Ala Phe Gln Ile Cys		
340	345	350
Gln Lys Lys Ala Lys Pro Gln Glu Ala Tyr Ser Leu Arg Ala Lys Arg		
355	360	365
Asn Ile Val Ile Asn Thr Ser Gly Leu Leu Val Gln Glu Pro Val Ser		
370	375	380
Gln Asn Pro Gly Gly Glu Asn Leu Gly Cys Gly Lys Ser Ala Asp Asn		
385	390	395
Pro His Arg Asn Pro		
405		

SEQ ID NO: 4

Length: 1903

Type: DNA

Organism: Homo sapiens

Sequence: 4

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SEQ ID NO: 5

Length: 1228

Type: DNA

Organism: Mus musculus

Sequence: 5

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tatctccacc agccccaaagt ggcagctgtc ttcatcagct cctacccct gatcttgtc 180  
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atgtatgca a ggttgggc ttcccttcc aagacggcag cacactgcac aggcaagcag 780  
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1228

FIGURE 1

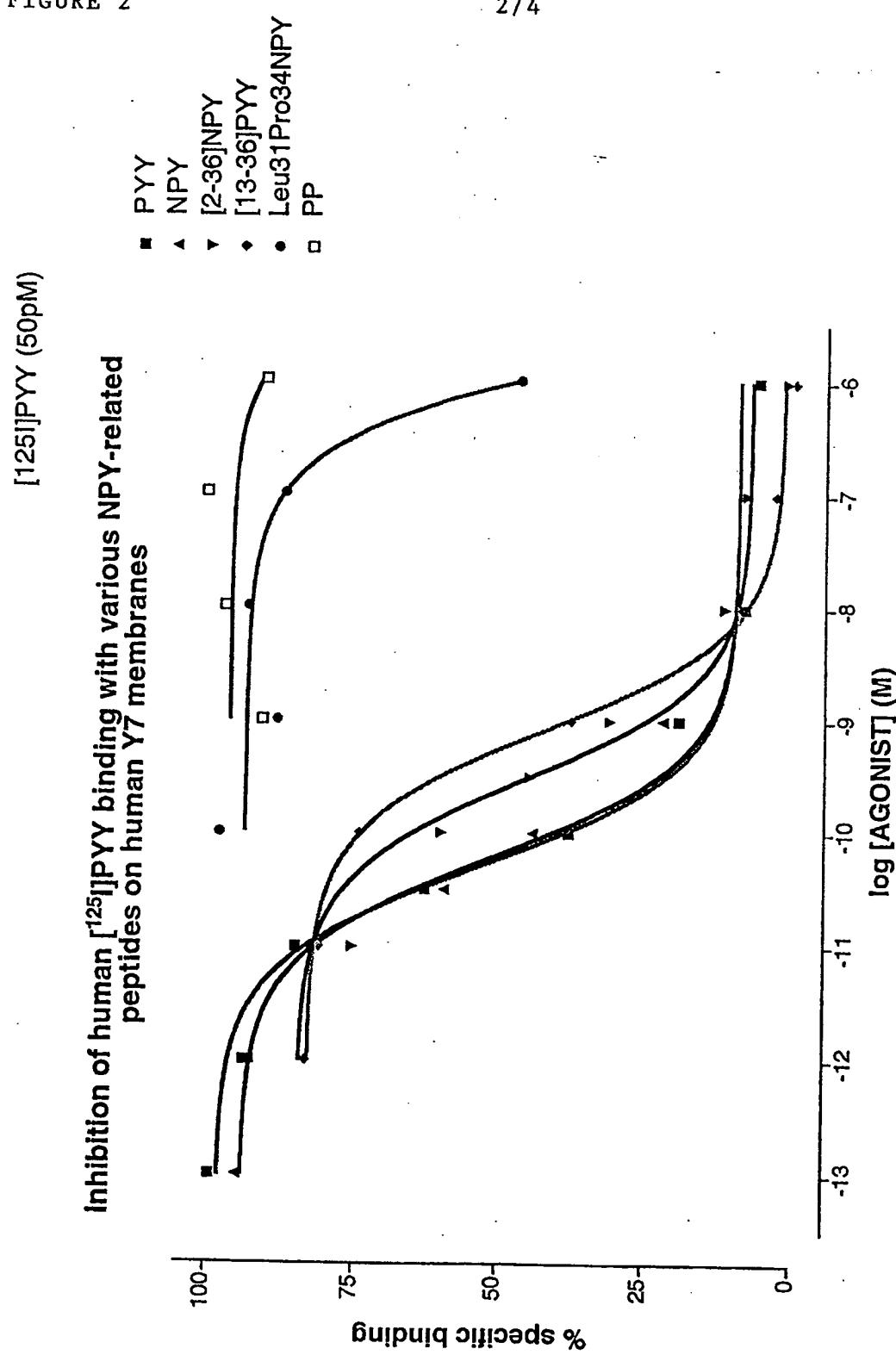
1 / 4

### Human neuropeptide Y - Y7 sequence alignment

hy1p	1	M G P [I] G A B A D E N Q T V E E M K V E Q Y G P Q I	16
hy2p	1	MG P [I] G A B A D E N Q T V E E M K V E Q Y G P Q I	26
hy7p	1	- M F I M N E K W D T N S S E N W H P I W N V N D I	25
hy1p	17	N F S E K N A Q L L A F E N D D C H L P L A M I F T L A L A Y G A V I	52
hy2p	27	T P R G E L V P D P E P E B L I D S T K L I E V Q V V I L A Y C S I L	62
hy7p	26	K H H L Y S D I N I T Y V N Y Y L H Q P - Q M A A I F I I I S Y F L F F	60
hy1p	53	L G V S G N L A L I I L K Q K E M R N V T N I L I I V N I S F S D L L	88
hy2p	63	L G V I G N S L V I H V V I K F K S M R T V T N F F I A N L A V A D L L	98
hy7p	61	C M M G N T V V C F I V M R N K H M H T V T N L F I L N L A I S D L L	96
hy1p	89	V A I M C L P F T I F V I Y T L M D H W V F G E A M C K L N P F V Q C V S I	124
hy2p	99	V N T L C L P F T I L T Y T L M G E W K M G P V L C H L V P Y A Q G L A M	134
hy7p	97	V G I F C M P I T L L D N I I A G W P F G N T M C K I S G L V O G I S V	132
hy1p	125	T V S I I F S L V L I A V E R H O L T I I N P R G W R P R N N R H A Y V G I A	160
hy2p	135	Q V S T I I T L T V I A L D R H R C I V Y H L E S K I S K R I S F L I I G	170
hy7p	133	A A S V E I I L V A I A V D R F Q C V V Y P F K P K L T I K T A F V I I M	168
hy1p	161	V I W V I L A V A S S L P F L Y Q V M T D E P F Q N V T I D - - - A Y K	193
hy2p	171	L A W G I S A L L A S P L A - - - - - H R E Y S I I E I I P D F	198
hy7p	169	I I W V I L A I T I M S P S A V M L H V Q E E K Y Y R V R I N S Q N K T S	204
hy1p	194	D K Y V C F D Q F P S D S H R L S Y L L V - - - L Q Y F G P I C F	226
hy2p	199	E I V A C T E K W P G E E K S I Y G I V Y S I S S L L I L Y V L P U G I	234
hy7p	205	P V Y W C R E D W P N Q E M R K I Y V L F A N I - - - Y L A P L S L	237
hy1p	227	I I F I C Y F K I Y R L K R R N N - - - M M D K M R D N K Y R S S E I K	259
hy2p	235	I I S F S Y T R I W S K L K N H V S P - - - G A A N D H Y H Q R R Q K T I K	268
hy7p	238	I I V I M Y G R I G I S U F R A A V P H T G R K N Q E Q W H V V S R K K Q	273
hy1p	260	R I N I M L S I N V A F A V C W L P T I F I N T V F D W - - - N H Q I I	293
hy2p	269	- - - M L V C V V V V F A V S W L P L H A Q L A V D I - - - D S e V L	298
hy7p	274	K I I K M L S I V A L L F I L S W L P I W T L M M L S D Y A D L S P N E	309
hy1p	294	A T C N H N L F I L L C H L T I A M I S T C V N P I F Y G E L N K N E Q R	329
hy2p	299	D L K E Y K I F I T V F H I I A M C S I F A N P L L Y G W M N S N Y R K	334
hy7p	310	L Q I I I N I Y I Y P F A W L A F G N S S V N P I I I Y G H F N E N F R R	345
hy1p	330	D L Q F F F N F C D F R S R D D D Y E T I A M S T M H T D V S K I T S L K	365
hy2p	335	A P L S A P R C E Q R L D A I H S E V S V I F K A K K N L E V R K N S G	370
hy7p	346	G F Q E A P Q L Q L C Q K R A K P M E A Y T L K A K S H V L I N T S N Q	381
hy1p	366	Q A S P V A E K K I N N N D D N E K I	384
hy2p	371	P N D S F E A T N V	381
hy7p	382	L V Q E S T P Q N P H G E T L L Y R K S A E N P N R N	408

FIGURE 2

2/4



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FIGURE 3

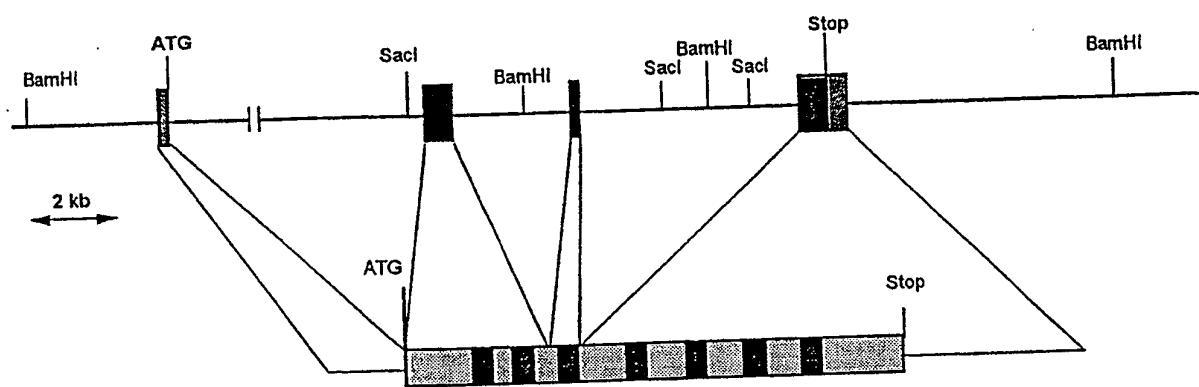
**Mouse NPY-Y7 Gene**

FIGURE 4

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## Human-Mouse NPY Y7 Receptor Alignment

hy7	1	M F I M N E K W D T N S S E N W H P I W N V N D T K H H L Y S D I N I T Y V	38
mY7	1	M S T M S E K W D S N S S E S W N H I W S G N D T Q H H W Y S D I N I T Y Y	38
hy7	39	N Y Y L H Q P Q Y A A I F I S Y F L I F F L C M M G N T V V C F I V M R N	76
mY7	39	N Y Y L H Q P Q Y A A V F I S S Y L L F V L C M V G N T V V C F I V I R N	76
hy7	77	K H M H T V T N L F I I N L A I S D I L L V G I F C M P I T L L D N I I A G W	114
mY7	77	R H M H T V T N F L I I N L A I S D I L L V G I F C M P I T L L D N I I A G W	114
hy7	115	P F G N T M C K I S G L V Q G I S V A A S V F T L V A I A V D R F Q C V V Y	152
mY7	115	P F G S S M C K I S G L V Q G I S V A A S V F T L V A I A V D R F R C V V Y	152
hy7	153	P F K P K L T I K T A R V I I M I I W V L A I T I M S P S A V M L H V Q E E	190
mY7	153	P F K P K L T V K T A R V T I V I I W G L A I A I M T P S A I M L H V Q E E	190
hy7	191	K Y Y R V R L N S Q N K T S P V Y W C R E D W P N Q E M R K I Y T T V L F A	228
mY7	191	K Y Y R V R L S S H N K T S T V Y W C R E D W P R H E M R R I Y T T V L F A	228
hy7	229	N I Y L A P L S L I V I M Y G R I G I S L F R A A V P H T G R K N Q E Q W H	266
mY7	229	I I Y L A P L S L I V I M Y A R I G A S L F K T A A H C T G - - K Q R P V Q	264
hy7	267	V V S R K K Q K I I K M I I I V A L L F I I S W L P L W T L M M I L S D Y A D	304
mY7	265	C M Y Q E K Q K V I K M I I T V A L L F I I S W L P L W T L M M I L S D Y T D	302
hy7	305	L S P N E I Q I I N I Y I Y P F A H W L A F G N S S V N P I I Y G F E N E N	342
mY7	303	L S P N K I R I I N I Y I Y P F A H W L A F C N S S V N P I I Y G F E N E N	340
hy7	343	F R R G F Q E A F Q L L Q L C Q K R A K P M E A Y T I K A K S H V L I N T S N	380
mY7	341	F R N G F Q D A F Q I - - C Q K K A K P Q E A Y S I R A K R N I V I N T S G	376
hy7	381	Q L V Q E S T F Q N P H G E T I L Y R K S A E N P N R N	408
mY7	377	L L V Q E P V S Q N P G G E N I G C G K S A D N P H R N P	405

## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/AU 99/00523

## A. CLASSIFICATION OF SUBJECT MATTER

Int Cl<sup>6</sup>: C12N 15/12 C07K 14/72, 16/28 C12 19/34 G01N 33/58

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
DGENE and WPAT SEE BELOWDocumentation searched other than minimum documentation to the extent that such documents are included in the fields searched  
DNA DATA BASES (SWISS PROT, GENBANK, EMBL, PIR) SEE BELOWElectronic data base consulted during the international search (name of data base and, where practicable, search terms used)  
DNA DATABASES: SEQ ID NOS 2 and 3 (entire sequences) and amino acids 1-15 of SEQ ID NOS 2 and 3  
DGENE: SEQ ID NO 2 (1-175 and 1-15) and SEQ ID NO 1 WPAT: (NPY receptor) or (neuropeptide Y receptor)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
PX	EP, A 0 884 387 (SMITHKLINE BEECHAM CORPORATION) 16 December 1998 See page 6 and table 2 in particular	1-26
PX	Biochem. Biophys. Res. Comm. 256, pages 352-6 (1999) "Sequence and tissue distribution of a novel G-protein-coupled receptor expressed prominently in human placenta." Cikos, S. et al. See the entire document.	1-26

 Further documents are listed in the continuation of Box C See patent family annex

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier application or patent but published on or after the international filing date
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- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

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"X" document of particular relevance, the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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"&" document member of the same patent family

Date of the actual completion of the international search  
14 July 1999Date of mailing of the international search report  
21 JUL 1999Name and mailing address of the ISA/AU  
AUSTRALIAN PATENT OFFICE  
PO BOX 200  
WODEN ACT 2606  
AUSTRALIA  
Facsimile No.: (02) 6285 3929Authorized officer  
**TERRY MOORE**  
Telephone No.: (02) 6283 2569

**INTERNATIONAL SEARCH REPORT**

International application No.  
PCT/AU 99/00523

<b>C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT</b>		
<b>Category*</b>	<b>Citation of document, with indication, where appropriate, of the relevant passages</b>	<b>Relevant to claim No.</b>
A	Trends in Neuroscience 20(7) pages 294-8 (1997) "Y-receptor subtypes-how many more?" Blomqvist, A.G. and Herzog, H. See the entire document.	1-26
A	WO, A 96 34877 (HUMAN GENOME SCIENCES, INC.) 7 November 1996 See the entire document.	1-26

**INTERNATIONAL SEARCH REPORT**  
Information on patent family members

International application No.  
PCT/AU 99/00523

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report	Patent Family Member			
WO 96 34877	AU	24707/95	EP	0 828 751
END OF ANNEX				